

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 12:53:40 ; Search time 14 Seconds
(without alignments)

1724.230 Million cell updates/sec

Title: US-09-635-949-34

Perfect score: 3289

Sequence: 1 MDPFLALVLYSSLYLQAAE.....TGRIGLDVSLKKHCSEER 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	406.5	12.4	2871	1 FBN1_BOVIN	P98133 bos taurus
2	402	12.2	1221	1 FBL2_MOUSE	P37889 mus musculus
3	398.5	12.1	2871	1 FBN1_MOUSE	Q61554 mus musculus
4	397.5	12.1	2911	1 FBN2_HUMAN	P35556 homo sapien
5	397	12.1	2907	1 FBN2_MOUSE	Q61555 mus musculus
6	395.5	12.0	2871	1 FBN1_HUMAN	P35555 homo sapien
7	381.5	11.6	1184	1 FBL2_HUMAN	P98095 homo sapien
8	371	11.3	2871	1 FBN1_PIG	O9TV36 sus scrofa
9	353.5	10.7	443	1 FBL4_HUMAN	O95967 homo sapien
10	346.5	10.5	443	1 FBL4_CRICK	O55058 cricetus
11	343	10.4	703	1 FBL1_HUMAN	P23142 homo sapien
12	333.5	10.1	684	1 FBL1_CHICK	O73775 gallus gall
13	332.5	10.1	443	1 FBL4_MOUSE	Q9WVJ9 mus musculus
14	332	10.1	705	1 FBL1_MOUSE	O98879 mus musculus
15	330.5	10.0	448	1 FBL5_MOUSE	Q9WVH9 mus musculus
16	330.5	10.0	448	1 FBL5_RAT	Q9WVH8 rattus norv
17	329	10.0	835	1 CD97_HUMAN	P48960 homo sapien
18	327	9.9	652	1 CD93_HUMAN	Q9NPY3 homo sapien
19	327	9.9	956	1 MTN2_HUMAN	O00339 homo sapien
20	326.5	9.9	448	1 FBN2_HUMAN	Q9UBX5 homo sapien
21	325	9.9	712	1 FBL1_CAEL	O77469 caenorhabdi
22	322.5	9.8	956	1 MTN2_MOUSE	O08746 mus musculus
23	314.5	9.6	2556	1 NTC1_HUMAN	P46531 homo sapien
24	311	9.5	1403	1 NID2_MOUSE	O88322 mus musculus
25	310.5	9.4	2524	1 NOTC_XENLA	P21783 xenopus lae
26	308	9.4	2531	1 NTC1_MOUSE	Q01705 mus musculus
27	306.5	9.3	1247	1 NIDO_HUMAN	P14543 homo sapien
28	301	9.2	493	1 FBL3_RAT	O35568 rattus norv
29	297	9.0	2531	1 NTC1_RAT	Q07008 rattus norv
30	296	9.0	1712	1 LTB1_RAT	Q00918 rattus norv
31	295.5	9.0	1394	1 LTB5_HUMAN	P22064 homo sapien
32	295.5	9.0	1595	1 FBL1_HUMAN	O14766 homo sapien
33	295	9.0	493	1 FBL3_HUMAN	Q12805 homo sapien

34	293.5	8.9	2321	1 NTC3_HUMAN	Q9UM47 homo sapien
35	290.5	8.8	1964	1 NTC4_MOUSE	P16595 mus musculus
36	290	8.8	2003	1 NTC4_HUMAN	Q99466 homo sapien
37	287	8.7	1245	1 NIDO_MOUSE	P10493 mus musculus
38	286.5	8.7	931	1 EMRI_MOUSE	Q61549 mus musculus
39	286	8.7	2437	1 NTC1_BRARE	P46530 brachydanio
40	285.5	8.7	810	1 NELL_RAT	Q62919 rattus norv
41	285.5	8.7	1375	1 NID2_HUMAN	Q14112 homo sapien
42	281	8.5	644	1 CD93_MOUSE	O89103 mus musculus
43	281	8.5	2318	1 NTC3_MOUSE	Q61982 mus musculus
44	281	8.5	2319	1 NTC3_RAT	Q9L172 rattus norv
45	279.5	8.5	2703	1 NOTC_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1

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FBN1_BOVIN          STANDARD;          PRT;   2871 AA.
ID   FBN1_BOVIN
AC   P98133;
DT   01-OCT-1996 (Rel. 34, Created)
DI   01-OCT-1996 (Rel. 34, Last sequence update)
DE   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Fibrillin 1 precursor (MP340).
GN   FBN1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=95137597; PubMed=7835900;
RA   Tilstra D.J., Potter K.A., Hyers P.H.;
RT   "Sequence of the coding region of the bovine fibrillin cDNA and
RT   localization to bovine chromosome 10.";
RL   Genomics 23:480-485(1994).
RN   [2]
RP   PARTIAL SEQUENCE.
RX   MEDLINE=96132851; PubMed=8557636;
RA   Gibson M.A., Hatzinikolas G., Kumaratilake J.S., Sandberg L.H.,
RA   Nicholl J.K., Sutherland G.R., Cleary E.G.;
RT   "Further characterization of proteins associated with elastic fiber
RT   microfibrils including the molecular cloning of MAGP-2 (MP25).";
J. Biol. Chem. 271:1096-1103(1996).
CC   !- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
CC   THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
CC   LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
CC   !- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
CC   FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
CC   MICROFIBRILS.
CC   !- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.
CC   !- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.

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EMBL; L28748; AAA74122.1; -.
DR   HSRP; P35555; IAPJ
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001438; EGF_II.
DR   InterPro; IPR002212; Fibril-assoc.
DR   Pfam; PF00008; EGF; 46.
DR   Pfam; PF00683; TB; 9.

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DR PRINTS: PR00010; EGFBL00D.
 DR SMART; SM00179; EGF_CA: 42.
 DR SMART; SM00001; EGF_Like: 4.
 DR PROSITE; PS00010; ASX_HYDROXYL: 43.
 DR PROSITE; PS00022; EGF_1: 2.
 DR PROSITE; PS01186; EGF_2: 38.
 DR PROSITE; PS01187; EGF_CA: 43.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 Repeat; Signal; Multigene family.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 2871 FIBRILLIN 1.
 FT DOMAIN 81 112 EGF-LIKE 1.
 FT DOMAIN 115 146 EGF-LIKE 2.
 FT DOMAIN 147 178 EGF-LIKE 3.
 FT DOMAIN 246 287 EGF-LIKE 4.
 FT DOMAIN 288 329 EGF-LIKE 5.
 FT REPEAT 330 390 TGFBRP 1.
 FT DOMAIN 392 446 PRO-RICH.
 FT DOMAIN 449 489 EGF-LIKE 6.
 FT DOMAIN 490 529 EGF-LIKE 7.
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CC	DR	EMBL; X75285; CAA53040.1; -	
CC	DR	EMBL; AF135253; AAD34456.1; JOINED.	
CC	DR	EMBL; AF135239; AAD34456.1; JOINED.	
CC	DR	EMBL; AF135240; AAD34456.1; JOINED.	
CC	DR	EMBL; AF135241; AAD34456.1; JOINED.	
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CC	DR	EMBL; AF135252; AAD34456.1; JOINED.	
CC	DR	PIR; A49457; A49457.	
CC	DR	HSP; P00736; IAPQ.	
CC	DR	MGD; MG1-95488; Pbin2.	
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CC	DR	InterPro: IPR000152; Asx_hydroxyl.	
CC	DR	InterPro: IPR000561; EGF-like.	
CC	DR	InterPro: IPR001881; EGF_CA.	
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CC	DR	PROSITE; PS01177; ANAPHYLATOXIN_1; 3.	
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CC	DR	PROSITE; PS01187; EGF_CA; 10.	
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CC	KW	Calcium-binding; Alternative splicing; Repeat.	
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CC	FT	CHAIN 27 1221	FIRULIN-2.
CC	FT	DOMAIN 27 434	N.
CC	FT	DOMAIN 27 176	SUBDOMAIN NA (CYS-RICH).
CC	FT	DOMAIN 177 434	SUBDOMAIN NB (CYS-FREE).
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CC	FT	DOMAIN 594 635	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 669 708	EGF-LIKE 2.
CC	FT	DOMAIN 709 755	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 756 800	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 801 846	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 847 894	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 895 937	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 938 979	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 980 1018	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 1019 1061	EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 1062 1106	EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
CC	FT	DOMAIN 1111 1221	DOMAIN 111.
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 FT GP (IN REF. 2).
 FT CONFLICT 348 348 S -> L (IN REF. 2).
 FT CONFLICT 507 507 Q -> Q (IN REF. 2).
 FT CONFLICT 1102 1102 Q -> E (IN REF. 2).
 SQ SEQUENCE 1221 AA; 131818 MW; 87DB2A10A8FDC45F CRC64;
 Query Match 12.2%; Score 402; DB 1; Length 1221;
 Best local similarity 36.6%; Pred. NO. 4.4e-16;
 Matches 93; Conservative 29; Mismatches 92; Indels 40; Gaps 14;
 QY 80 RCKIGE-CI--GPNKCKHPGVA---GKTGLOVNEGLKP-RCKIRCMNTYGSYK 130
 DB 905 RCGHQQLCYMLPSYRCDCXKPGQRIAFGHTCIDV-NECWSPGRI-COHTCENTPGSYRC 963
 QY 131 YCLNGYMLPDGSS-CSSALTCGSMANQYGGDVYKGCQCPSPGLQAPDGRCTCVDDVE 189
 DB 964 SCAAGFLAADGKHCEVDNECETRCSCDEANITYGSQCYC-RQGYLAEDGHTCTDIDE 1022
 QY 190 CATGRASCPHROCVNTFGSYICKC-HKGFOLMYIGCKYQCHDIDKCSLGOYOCSSPARC 248
 DB 1023 CAQAGAGLCTER-CVNVPGSYQACPEQGYTMNANG--RSCKDLDECALGTINCSAEATC 1079
 QY 249 YNVRSYKCY--KCKEY-----QDGLTCVYIPKVMIEPSG-----PIH 285
 DB 1080 HNIQSPRCRLRFDCPPNVVVSQTKCHRTTCQDITHCQISPARITHYQLNPFQGLLVPAH 1139
 QY 286 VPK-GNCTILKGD 298
 DB 1140 IFRIGPAPAFAGDT 1153
 RESULT 3
 FBNI_MOUSE
 ID FBNI_MOUSE STANDARD; PRT: 2871 AA.
 AC Q61554; Q60826;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBNI OR FBNI-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95130561; PubMed-7829516;
 RA Yin W., Germiller J., Sanquinetti C., Smiley E., Panfilian T.,
 Pereira L., Ramirez P., Honadio J.;
 RT "Primary structure and developmental expression of Fbn 1, the mouse
 fibrillin gene.";
 RL J. Biol. Chem. 270:1798-1806(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CD-1; TISSUE-Kidney;
 RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC -!- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
 CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
 CC MICROFIBRILS (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
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 DR EMBL; I29454; AAA56840.1; .
 DR EMBL; U22493; AAA64217.1; .
 DR HSSP; P35555; IAP1.
 DR MGD; MGI-95489; Fbn1.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR002212; Fibrill-assoc.
 DR Pfam; PF00008; EGF; 46.
 DR Pfam; PF00683; TB; 9.
 DR SMART; SM00179; EGF_CA; 42.
 DR SMART; SM00001; EGF_Like; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 38.
 DR PROSITE; PS01187; EGF_CA; 43.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF like domain;
 KW Repeat; Signal; Multigene family.
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 FT CHAIN 28 2871 FIBRILLIN 1.
 FT DOMAIN 81 112 EGF-LIKE 1.
 FT DOMAIN 115 146 EGF-LIKE 2.
 FT DOMAIN 147 178 EGF-LIKE 3.
 FT DOMAIN 246 287 EGF-LIKE 4, CALCIUM-BINDING.
 FT DOMAIN 288 329 EGF-LIKE 5, CALCIUM-BINDING.
 FT DOMAIN 330 401 TGFBP 1.
 FT DOMAIN 402 446 PRO-RICH.
 FT DOMAIN 449 489 EGF-LIKE 6.
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 FT DOMAIN 1113 1154 EGF-LIKE 17, CALCIUM-BINDING.
 FT DOMAIN 1155 1196 EGF-LIKE 18, CALCIUM-BINDING.

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FT DOMAIN 1197 1237 EGF-LIKE 19, CALCIUM-BINDING. 921 935 BY SIMILARITY.
FT DOMAIN 1238 1279 EGF-LIKE 20, CALCIUM-BINDING. 937 950 BY SIMILARITY.
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FT DOMAIN 1322 1362 EGF-LIKE 22, CALCIUM-BINDING. 1039 1053 BY SIMILARITY.
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Query Match 12.1%: Score 398.5; DB 1; Length 2871;
Best Local Similarity 31.7%; Pred. No. 1.4e-15;
Matches 104; Conservative 33; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRYG-----GRIDCCWGMARQSWGQCOPPYVLRQRIARI-----RCOLKAVCQPRCKHG 84
DB 1123 LCRGGICHNTGTYRC-----ECPPGHQLSPNISACIDINECELSA---NLCPHG 1169
QY 85 EC---IGPNKCKCHPCYACK---TCIOVLNKCGLKPRCKHRCNMNTYGSYKCYCLNGYM 137
DB 1170 RCVNLIGKYQCACNPGYHTDRLFCVDI-DKCSLMNGGCTFTCTNSDGSVECSQCPGFA 1228
QY 138 LMPD-GSCSSALTC--SMANGCYG-CDVVKGQIRQCPSGLQAPDGRTCVDV----- 187
DB 1229 LMPDQRCTDHDQEDNPNICDGGGCTNIPGEYKCLC-YDGFMAFDMKTCVDVNECDLN 1287
QY 188 -----DKCATGRASCPHPRQCVNTFGSYI 211
DB 1288 PNICLSGTGTCNTKGSFICHDMGYSKKGKTKCTDINECEIGHNCGRHAVCTNTAGSEFK 1347
QY 212 CKCHKGFIDLMIYIGGKYQCHDIDECSLGOYOCSSPFCYVNRKSYCKCKEYQGGILTCV 271
DB 1348 CSCSPG----WIGDGIKCTDLDDECSNTHMCSQHADCKNTMGSRCLCKDGYTGDFGTCT 1403
QY 272 YIPKVMIEPSPGPIHPKNGTILKGDG 299
DB 1404 DLD----ECSENLNL-CGNGQCLNAPGG 1426
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RESULT 4
 FBN2_HUMAN STANDARD; PRT; 2011 AA.
 AC P35556;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Fibrillin-2 precursor.
 GN FBN2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-94165150; PubMed-8120105;
 RX Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguinetti C.,
 RA Bonadio J., Mechem R.P., Ramirez F.,
 RT "Structure and expression of fibrillin-2, a novel microfibrillar
 component preferentially located in elastic matrices";
 RT J. Cell Biol. 124:855-863(1994).
 RL [2]
 RN SEQUENCE OF 752-1505 FROM N.A.
 RP MEDLINE-91304567; PubMed-1852206;
 RX Lee H., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
 RA Tsipouras P., Ramirez F., Hollister D.,
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to
 RT two different fibrillin genes";
 RL Nature 352:330-334(1991).
 [3]
 RN VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964.
 RP MEDLINE-96083599; PubMed-7493032;
 RX Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.;
 RA "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder,
 RT congenital contractual arachnoidectyly";
 RL Nat. Genet. 11:456-458(1995).
 [4]
 RN VARIANTS CCA HIS-1114.
 RP MEDLINE-98407789; PubMed-9737771;
 RX Babcock D., Gasner C., Francke U., Maslen C.;
 RA "A single exon skipping that results in an asp-to-his substitution and
 RT partial exon skipping in a family with congenital contractual
 RT arachnoidectyly";
 RL Hum. Genet. 103:22-28(1998).
 [5]
 RN VARIANTS CCA PHE-1141 AND TRP-1252.
 RP MEDLINE-20259236; PubMed-10797416;
 RX Belich S., Zhou G., Wang M., Der Kaloustian V.M., Pagon R.A.,
 RA Godfrey M.;
 RT "Two novel fibrillin-2 mutations in congenital contractual
 RT arachnoidectyly";
 RL Am. J. Med. Genet. 92:7-12(2000).
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE
 CC THE EARLY PROCESS OF ELASTIC FIBER ASSEMBLY.
 CC -1- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL
 CC ARACHNOIDECTYLY (CCA) (ALSO KNOWN AS BEAUS SYNDROME). CCA IS
 CC PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT AFFECT THE
 CC AORTA AND THE EYES.
 CC -1- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
 CC -----
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 DR FBN2; U03272; AAA18950.1;
 DR EMBL; X62009; -; NOT_ANNOTATED_CDS.
 DR PIR; S17063; S17063.
 DR PIR; S31101; S31101.
 DR HSSP; P35555; 1EMN.
 DR Genew; HGNC:3604; FBN2.
 DR MIM; 121050; -.
 DR InterPro; IPR000152; ASX_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR001438; EGF-II.
 DR InterPro; IPR002212; Fibrill-assoc.
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 DR Pfam; PF00683; TH; 9.
 DR PRINTS; PR00010; EGFHLODP.
 DR SMART; SM00179; EGF_CA; 43.
 DR SMART; SM00001; EGF_Like; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 37.
 DR PROSITE; PS01187; EGF_CA; 42.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family; Disease mutation; Polymorphism.
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 FT EGF-LIKE 49

FT DOMAIN 2570 2612 EGF-LIKE 44, CALCIUM-BINDING.
 FT DOMAIN 2613 2652 EGF-LIKE 45, CALCIUM-BINDING.
 FT DOMAIN 2653 2693 EGF-LIKE 46, CALCIUM-BINDING.
 FT DOMAIN 2694 2733 EGF-LIKE 47, CALCIUM-BINDING.
 FT DISULFID 115 124 BY SIMILARITY.
 FT DISULFID 119 130 BY SIMILARITY.
 FT DISULFID 132 141 BY SIMILARITY.
 FT DISULFID 149 159 BY SIMILARITY.
 FT DISULFID 153 164 BY SIMILARITY.
 FT DISULFID 166 175 BY SIMILARITY.
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 FT DISULFID 497 509 BY SIMILARITY.
 FT DISULFID 504 518 BY SIMILARITY.
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 FT DISULFID 620 631 BY SIMILARITY.
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 FT DISULFID 642 655 BY SIMILARITY.
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 FT DISULFID 1141 1155 BY SIMILARITY.
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 FT DISULFID 1168 1182 BY SIMILARITY.
 FT DISULFID 1184 1197 BY SIMILARITY.
 FT DISULFID 1203 1215 BY SIMILARITY.
 FT DISULFID 1210 1224 BY SIMILARITY.

Query Match 12.1%; Score 397.5; DB 1; Length 2911;
 Best local Similarity 35.0%; Pred. No. 1.6e-15;
 Matches 84; Conservative 31; Mismatches 72; Indels 53; Gaps 9;

QY 81 CKIGEC---IGPNKKCHPGYAG-----KTCIQVNEGLKPRPKRCHRCNMTYGSYKCYCL 133
 DB 1210 CRNGKVNMTGTYQCSNFGYQATPDQGTCTDI-DECLMNGGCDTQCTNSEGSYECSCS 1268
 QY 134 NGYMLMPDG-SCSSALTC--SMANCOYG-CDVVKGOIRCOQSPGLQAPDGTCTVDVDF 189
 DB 1269 EGVALPMDGRSCADIDECENPNPDICGGQCTNIPGEYRCLC-YDGFPMASNDKTKCIDVNE 1327
 QY 190 CATGRACSPFRQCVNFTGYSICKCHKGFGLM----- 221
 DB 1328 CDLNSNIC-WFGEENWTGKSFICHOLGLYSVKKGTTCCTDVIDDFCFIARNDCHASCLNI 1386

QY 222 -----YIGCKYQCHDIDECISIQOYQCSSPARCYNVRGSKYKCKKGYQDGLTC 270
 DB 1387 PGSEKCSREGWIGNGIRKIDIDECNSGTHQCSINAQCVNTPGSYRCACSEGTGDTGFTC 1446

RESULT 5
 FBN2_MOUSE
 ID FBN2_MOUSE STANDARD: PRT: 2907 AA.
 AC Q61555; Q63957;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrillin 2 precursor.
 GN FBN2 OR FBN-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP MEDLINE-95263670; PubMed=7744963;
 RX Zhang H., Hu W., Ramirez F.;
 RA "Developmental expression of fibrillin genes suggests heterogeneity
 of extracellular microfibrils.";
 RT J. Cell Biol. 129:1165-1176(1995).
 RN [2]
 RP MEDLINE-94140368; PubMed=8307578;
 RX Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,
 RA Francke U.;
 RT "Fibrillin genes map to regions of conserved mouse/human synteny on
 mouse chromosomes 2 and 18.";
 RL Genomics 18:667-672(1993).
 CC - FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC - LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC - SIMILARITY: CONTAINS 7 EGF-LIKE DOMAINS.
 CC - SIMILARITY: CONTAINS 47 TGF-BETA BINDING PROTEIN DOMAINS.
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 EMBL; L39790; AAA74908.1; -;
 EMBL; S69359; AAC60685.1; -;
 HSSP; P35555; IENN.
 DR MGD; MGI:95490; Fbn2.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00683; TB; 9.
 DR PRINTS; P300010; EGFRIOOD.
 DR SMART; SM00179; EGF_CA; 43.
 DR SMART; SM00001; EGF_Like; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 36.
 DR PROSITE; PS01187; EGF_CA; 43.
 DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 2907 FIBRILLIN 2.
 FT DOMAIN 111 142 EGF-LIKE 1.
 FT DOMAIN 145 176 EGF-LIKE 2.
 FT DOMAIN 176 208 EGF-LIKE 3.

TT	DOMAIN	276	317	EGF-LIKE 4, CALCIUM-BINDING.
TT	DOMAIN	318	359	EGF-LIKE 5, CALCIUM-BINDING.
TT	REPEAT	360	426	TGFBP 1.
TT	DOMAIN	487	527	EGF-LIKE 6.
TT	DOMAIN	528	567	EGF-LIKE 7.
TT	DOMAIN	568	609	EGF-LIKE 8, CALCIUM-BINDING.
TT	DOMAIN	610	650	EGF-LIKE 9, CALCIUM-BINDING.
TT	DOMAIN	651	691	EGF-LIKE 10, CALCIUM-BINDING.
TT	REPEAT	692	760	TGFBP 2.
TT	DOMAIN	761	802	EGF-LIKE 11, CALCIUM-BINDING.
TT	DOMAIN	803	844	EGF-LIKE 12, CALCIUM-BINDING.
TT	DOMAIN	845	883	EGF-LIKE 13, CALCIUM-BINDING.
TT	DOMAIN	948	989	EGF-LIKE 14, CALCIUM-BINDING.
TT	REPEAT	990	1065	TGFBP 3.
TT	DOMAIN	1066	1107	EGF-LIKE 15, CALCIUM-BINDING.
TT	DOMAIN	1108	1150	EGF-LIKE 16, CALCIUM-BINDING.
TT	DOMAIN	1151	1192	EGF-LIKE 17, CALCIUM-BINDING.
TT	DOMAIN	1193	1234	EGF-LIKE 18, CALCIUM-BINDING.
TT	DOMAIN	1235	1275	EGF-LIKE 19, CALCIUM-BINDING.
TT	DOMAIN	1276	1317	EGF-LIKE 20, CALCIUM-BINDING.
TT	DOMAIN	1318	1359	EGF-LIKE 21, CALCIUM-BINDING.
TT	DOMAIN	1360	1400	EGF-LIKE 22, CALCIUM-BINDING.
TT	DOMAIN	1401	1441	EGF-LIKE 23, CALCIUM-BINDING.
TT	DOMAIN	1442	1483	EGF-LIKE 24, CALCIUM-BINDING.
TT	DOMAIN	1484	1524	EGF-LIKE 25, CALCIUM-BINDING.
TT	DOMAIN	1525	1565	EGF-LIKE 26, CALCIUM-BINDING.
TT	REPEAT	1566	1642	TGFBP 4.
TT	DOMAIN	1643	1684	EGF-LIKE 27, CALCIUM-BINDING.
TT	DOMAIN	1685	1726	EGF-LIKE 28, CALCIUM-BINDING.
TT	REPEAT	1727	1800	TGFBP 5.
TT	DOMAIN	1801	1842	EGF-LIKE 29, CALCIUM-BINDING.
TT	DOMAIN	1843	1884	EGF-LIKE 30, CALCIUM-BINDING.
TT	DOMAIN	1885	1926	EGF-LIKE 31, CALCIUM-BINDING.
TT	DOMAIN	1927	1965	EGF-LIKE 32, CALCIUM-BINDING.
TT	DOMAIN	1966	2008	EGF-LIKE 33, CALCIUM-BINDING.
TT	DOMAIN	2009	2048	EGF-LIKE 34, CALCIUM-BINDING.
TT	DOMAIN	2049	2090	EGF-LIKE 35, CALCIUM-BINDING.
TT	REPEAT	2091	2163	TGFBP 6.
TT	DOMAIN	2164	2205	EGF-LIKE 36, CALCIUM-BINDING.
TT	DOMAIN	2206	2245	EGF-LIKE 37, CALCIUM-BINDING.
TT	DOMAIN	2246	2286	EGF-LIKE 38, CALCIUM-BINDING.
TT	DOMAIN	2287	2330	EGF-LIKE 39, CALCIUM-BINDING.
TT	DOMAIN	2331	2372	EGF-LIKE 40, CALCIUM-BINDING.
TT	REPEAT	2373	2441	TGFBP 7.
TT	DOMAIN	2442	2483	EGF-LIKE 41, CALCIUM-BINDING.
TT	DOMAIN	2484	2524	EGF-LIKE 42, CALCIUM-BINDING.
TT	DOMAIN	2525	2563	EGF-LIKE 43, CALCIUM-BINDING.
TT	DOMAIN	2564	2606	EGF-LIKE 44, CALCIUM-BINDING.
TT	DOMAIN	2607	2646	EGF-LIKE 45, CALCIUM-BINDING.
TT	DOMAIN	2647	2687	EGF-LIKE 46, CALCIUM-BINDING.
TT	DOMAIN	2688	2727	EGF-LIKE 47, CALCIUM-BINDING.
TT	DSULFID	115	124	HY SIMILARITY.
TT	DSULFID	119	130	BY SIMILARITY.
TT	DSULFID	132	141	BY SIMILARITY.
TT	DSULFID	149	159	BY SIMILARITY.
TT	DSULFID	153	164	BY SIMILARITY.
TT	DSULFID	166	175	BY SIMILARITY.
TT	DSULFID	180	190	BY SIMILARITY.
TT	DSULFID	184	196	BY SIMILARITY.
TT	DSULFID	198	207	BY SIMILARITY.
TT	DSULFID	280	292	BY SIMILARITY.
TT	DSULFID	287	301	BY SIMILARITY.
TT	DSULFID	303	316	BY SIMILARITY.
TT	DSULFID	322	334	BY SIMILARITY.
TT	DSULFID	329	343	BY SIMILARITY.
TT	DSULFID	345	358	BY SIMILARITY.
TT	DSULFID	491	503	BY SIMILARITY.
TT	DSULFID	498	512	BY SIMILARITY.
TT	DSULFID	514	526	BY SIMILARITY.
TT	DSULFID	532	542	BY SIMILARITY.
TT	DSULFID	537	551	BY SIMILARITY.
TT	DSULFID	553	566	BY SIMILARITY.
TT	DSULFID	572	584	BY SIMILARITY.

[illegible]

RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.:
 RT "A novel fibrillin mutation in the Marfan syndrome which could
 RL disrupt calcium binding of the epidermal growth factor-like module.";
 RN Hum. Mol. Genet. 2:475-477(1993).
 RP
 RX VARIANTS MFS R-862; Y-1117; P-1137 AND F-1589, AND VARIANT A-1148.
 RM MEDLINE-94108431; PubMed-8281141;
 RA Tyan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gasner C.,
 RA Berg M.A., Miller D.C., Francke U.:
 RT "Mutation screening of complete fibrillin-1 coding sequence: report
 RL of five new mutations, including two in B-cysteine domains.";
 RN Hum. Mol. Genet. 2:1813-1821(1993).
 RP
 RX VARIANTS MFS GLY-217 AND ARG-2627.
 RM MEDLINE-95067970; PubMed-7977366;
 RA Karttunen L., Raghunath M., Leenqvist L., Peltonen L.:
 RT "A compound-heterozygous Marfan patient: two defective fibrillin
 RL alleles result in a lethal phenotype.";
 RN Am. J. Hum. Genet. 55:1083-1091(1994).
 RP
 RX VARIANT EL IYS-2447.
 RM MEDLINE-94245249; PubMed-8188302;
 RA Lonnqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
 RA Peltonen L.:
 RT "A novel mutation of the fibrillin gene causing ectopia lentis.";
 RL Genomics 19:573-576(1994).
 RN
 RX VARIANT MFS CYS-627.
 RM MEDLINE-94272487; PubMed-8004112;
 RA Hayward C., Rae A.B., Porteous M.E.M., Lozie L.J., Brock L.J.:
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains
 RL of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan
 RN syndrome patients.";
 RM Hum. Mol. Genet. 3:373-375(1994).
 RP
 RX VARIANT MFS CYS-122.
 RM MEDLINE-94314977; PubMed-8040326;
 RA Stahl-Hallenqren C., Ukkonen T., Kainulainen K., Kristofersson U.,
 RA Saxne T., Tornqvist K., Peltonen L.:
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth
 RL factor-like motifs of the FBN1 polypeptide is connected to a novel
 RN variant of Marfan syndrome.";
 RM J. Clin. Invest. 94:709-713(1994).
 RP
 RX VARIANT MFS TYR-1223.
 RM MEDLINE-94351682; PubMed-8071963;
 RA Hewett D.R., Lynch J.R., Child A., Sykes H.C.:
 RT "A new missense mutation of fibrillin in a patient with Marfan
 RL syndrome.";
 RM J. Med. Genet. 31:338-339(1994).
 RP
 RX VARIANT MFS HIS-1170.
 RM MEDLINE-95174777; PubMed-7870075;
 RA Hayward C., Porteous M.E.M., Brock D.J.H.:
 RT "A novel mutation in the fibrillin gene (FBN1) in familial
 RL arachnodactyly.";
 RM Mol. Cell. Probes 8:325-327(1994).
 RP
 RX VARIANTS MFS G-217; N-1023; R-1074; Y-1242; R-1513; E-2127; W-2151;
 RM K-2447 AND R-2511.
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.:
 RT "Mutations in the fibrillin gene responsible for dominant ectopia
 RL lentis and neonatal Marfan syndrome.";
 RN Nat. Genet. 6:64-69(1994).
 RP
 RX VARIANT SER-1127.
 RM
 RL
 RP

Query Match

Best local Similarity 12.0%; Score 395.5; DH 1; Length 2871;

Matches 103; Conservative 34; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRYG-----GRIDCGWNRQSWQCQPPYVLRORIARI-----RCQLKAVQPRCKKUG 84

Db 1123 LCRGGVCHINTGYSYR-----CLOVNFQGLKPRCKHRCNNTYSKYCYGLNGYM 1169
 QY 85 EC---ICPNKCKCHCYACKT---CLOVNFQGLKPRCKHRCNNTYSKYCYGLNGYM 147
 Db 1170 RCVNLEIGKYGCACNPGYHSTPDLFCVDI-DEGSMNGGCTETCTNSENSESGYSCGCGPA 1228
 QY 138 LMPD-GSCSSALTTC--SMANCOVG-CDVVKGOIRGQFSPGQLAFDRKTCVDV--- 187
 Db 1229 LMPDORSCTDIDECHEPNICDGGQCTNIPGHCRLC-YDGFMAHSDMKTCVIVNRCTDLN 1287
 QY 188 -----DECATGRASCPFRFGVNTFGSYI 211
 Db 1288 PNICLSGTCENTKGSFICHDMGYSGKKGKTCGTIDINEGEIARNGGKIAVCTNTAGSEK 1447
 QY 212 CCKCHKFDLMYLGCKYOCCHDIOFCSLGOYOCSSPANCYNVRGSKCKKRGYOCGELICV 271
 Db 1348 CSCSPG---WIGDGIKCTDLDECNSGTMCSQIADKXNTMGSYRGLKREGYTGEGFTT 1404
 QY 272 YIPKVMIEPSGPIHVPKNGNTILKGDGTG 299
 Db 1404 DLD-----ECSENLNL-CGNCQCLINAICG 1426
 RESULT 7
 FBL2.HUMAN STANDARD; PRT; 1184 AA.
 AC P98095;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrillin-2 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID:9606;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE-Fibroblast;
 RX MEDLINE-95104855; PubMed-7806230;
 RA Zhang R.-Z., Fan T.-C., Zhang Z.-Y., Mattei M. G., Timpl R.,
 RA Chu M.-L.;
 RT "Fibrillin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
 RL of the gene on human and mouse chromosomes.";
 CC Genomics 22:425-430(1994).
 CC
 CC -1- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
 CC -1- CALCIUM DEPENDENT.
 CC
 CC -1- SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED.
 CC
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX. COMPONENT OF BOTH
 CC -1- HASHMENT MEMBRANES AND OTHER CONNECTIVE TISSUES.
 CC
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, PLACENTA AND OVARY.
 CC
 CC -1- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
 CC
 CC -1- SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
 CC
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 DR FMHL; X82494; CAA57876.1; -;
 DR HSSP; P00736; IAPQ.
 DR Genew; HGNC:3601; FBLN2.
 DR MIM; 135821; -;
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR Pfam; PF000608; EGF; 7.
 DR Pfam; PF01821; ANATO; 2.

DK PRINTS; PRO0010; EGFRLDOP.
DR SMART; SM00179; EGF_CA; 40.
DR SMART; SM00001; EGF_LIKE; 6.
DR DR PROSITE; PS00010; ASX_HYDROXYL; 41.
DR DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR DR PROSITE; PS01186; EGF_2; 36.
DR DR PROSITE; PS01187; EGF_CA; 41.
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
Repeat; Signal; Multigene family.
FT SIGNAL 1 27 POTENTIAL
FT CHAIN 28 2871 FIBRILLIN 1.
FT DOMAIN 81 112 EGF-LIKE 1.
FT DOMAIN 115 146 EGF-LIKE 2.
FT DOMAIN 147 178 EGF-LIKE 3.
FT DOMAIN 246 287 EGF-LIKE 4.
FT DOMAIN 288 329 EGF-LIKE 5, CALCIUM-BINDING.
FT REPEAT 330 390 TGFBR 1.
FT DOMAIN 392 446 PRO-RICH.
FT DOMAIN 449 489 EGF-LIKE 6.
FT DOMAIN 490 529 EGF-LIKE 7, CALCIUM-BINDING.
FT DOMAIN 530 571 EGF-LIKE 8, CALCIUM-BINDING.
FT DOMAIN 572 612 EGF-LIKE 9, CALCIUM-BINDING.
FT DOMAIN 613 653 EGF-LIKE 10, CALCIUM-BINDING.
FT REPEAT 654 722 TGFBR 2.
FT DOMAIN 723 764 EGF-LIKE 11, CALCIUM-BINDING.
FT DOMAIN 765 806 EGF-LIKE 12, CALCIUM-BINDING.
FT DOMAIN 807 846 EGF-LIKE 13, CALCIUM-BINDING.
FT DOMAIN 910 951 EGF-LIKE 14, CALCIUM-BINDING.
FT REPEAT 952 1027 TGFBR 3.
FT DOMAIN 1028 1069 EGF-LIKE 15, CALCIUM-BINDING.
FT DOMAIN 1070 1112 EGF-LIKE 16, CALCIUM-BINDING.
FT DOMAIN 1113 1154 EGF-LIKE 17, CALCIUM-BINDING.
FT DOMAIN 1155 1196 EGF-LIKE 18, CALCIUM-BINDING.
FT DOMAIN 1197 1237 EGF-LIKE 19, CALCIUM-BINDING.
FT DOMAIN 1238 1279 EGF-LIKE 20, CALCIUM-BINDING.
FT DOMAIN 1280 1321 EGF-LIKE 21, CALCIUM-BINDING.
FT DOMAIN 1322 1362 EGF-LIKE 22, CALCIUM-BINDING.
FT DOMAIN 1363 1403 EGF-LIKE 23, CALCIUM-BINDING.
FT DOMAIN 1404 1445 EGF-LIKE 24, CALCIUM-BINDING.
FT DOMAIN 1446 1486 EGF-LIKE 25, CALCIUM-BINDING.
FT DOMAIN 1487 1527 EGF-LIKE 26, CALCIUM-BINDING.
FT REPEAT 1528 1605 TGFBR 4.
FT DOMAIN 1606 1647 EGF-LIKE 27, CALCIUM-BINDING.
FT DOMAIN 1648 1688 EGF-LIKE 28, CALCIUM-BINDING.
FT REPEAT 1689 1765 TGFBR 5.
FT DOMAIN 1766 1807 EGF-LIKE 29, CALCIUM-BINDING.
FT DOMAIN 1808 1848 EGF-LIKE 30, CALCIUM-BINDING.
FT DOMAIN 1849 1890 EGF-LIKE 31, CALCIUM-BINDING.
FT DOMAIN 1891 1929 EGF-LIKE 32, CALCIUM-BINDING.
FT DOMAIN 1930 1972 EGF-LIKE 33, CALCIUM-BINDING.
FT DOMAIN 1973 2012 EGF-LIKE 34, CALCIUM-BINDING.
FT DOMAIN 2013 2054 EGF-LIKE 35, CALCIUM-BINDING.
FT REPEAT 2055 2126 TGFBR 6.
FT DOMAIN 2127 2165 EGF-LIKE 36, CALCIUM-BINDING.
FT DOMAIN 2166 2205 EGF-LIKE 37, CALCIUM-BINDING.
FT DOMAIN 2206 2246 EGF-LIKE 38, CALCIUM-BINDING.
FT DOMAIN 2247 2290 EGF-LIKE 39, CALCIUM-BINDING.
FT DOMAIN 2291 2332 EGF-LIKE 40, CALCIUM-BINDING.
FT REPEAT 2333 2401 TGFBR 7.
FT DOMAIN 2402 2443 EGF-LIKE 41, CALCIUM-BINDING.
FT DOMAIN 2444 2484 EGF-LIKE 42, CALCIUM-BINDING.
FT DOMAIN 2485 2523 EGF-LIKE 43, CALCIUM-BINDING.
FT DOMAIN 2524 2566 EGF-LIKE 44, CALCIUM-BINDING.
FT DOMAIN 2567 2606 EGF-LIKE 45, CALCIUM-BINDING.
FT DOMAIN 2607 2647 EGF-LIKE 46, CALCIUM-BINDING.
FT DOMAIN 2648 2687 EGF-LIKE 47, CALCIUM-BINDING.
FT DISULFID 85 94 BY SIMILARITY.
FT DISULFID 89 100 BY SIMILARITY.
FT DISULFID 102 111 BY SIMILARITY.
FT DISULFID 119 129 BY SIMILARITY.
FT DISULFID 123 134 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 150 160 BY SIMILARITY.
FT DISULFID 154 166 BY SIMILARITY.
FT DISULFID 168 177 BY SIMILARITY.
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FT DISULFID 257 271 BY SIMILARITY.
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FT DISULFID 453 465 BY SIMILARITY.
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FT DISULFID 494 504 BY SIMILARITY.
FT DISULFID 499 513 BY SIMILARITY.
FT DISULFID 515 528 BY SIMILARITY.
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FT DISULFID 557 570 BY SIMILARITY.
FT DISULFID 576 587 BY SIMILARITY.
FT DISULFID 582 596 BY SIMILARITY.
FT DISULFID 598 611 BY SIMILARITY.
FT DISULFID 617 628 BY SIMILARITY.
FT DISULFID 623 637 BY SIMILARITY.
FT DISULFID 639 652 BY SIMILARITY.
FT DISULFID 727 739 BY SIMILARITY.
FT DISULFID 734 748 BY SIMILARITY.
FT DISULFID 750 763 BY SIMILARITY.
FT DISULFID 769 781 BY SIMILARITY.
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FT DISULFID 792 805 BY SIMILARITY.
FT DISULFID 811 821 BY SIMILARITY.
FT DISULFID 816 830 BY SIMILARITY.
FT DISULFID 842 845 BY SIMILARITY.
FT DISULFID 914 926 BY SIMILARITY.
FT DISULFID 921 935 BY SIMILARITY.
FT DISULFID 937 950 BY SIMILARITY.
FT DISULFID 1032 1044 BY SIMILARITY.
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FT DISULFID 1055 1068 BY SIMILARITY.
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FT DISULFID 1081 1095 BY SIMILARITY.
FT DISULFID 1097 1111 BY SIMILARITY.
FT DISULFID 1117 1129 BY SIMILARITY.
FT DISULFID 1124 1138 BY SIMILARITY.
FT DISULFID 1140 1153 BY SIMILARITY.
FT DISULFID 1159 1171 BY SIMILARITY.
FT DISULFID 1201 1212 BY SIMILARITY.
FT DISULFID 1208 1221 BY SIMILARITY.
FT DISULFID 1223 1236 BY SIMILARITY.
FT DISULFID 1242 1254 BY SIMILARITY.
FT DISULFID 1249 1263 BY SIMILARITY.
FT DISULFID 1265 1278 BY SIMILARITY.
FT DISULFID 1284 1296 BY SIMILARITY.
FT DISULFID 1291 1305 BY SIMILARITY.
FT DISULFID 1307 1320 BY SIMILARITY.
FT DISULFID 1326 1339 BY SIMILARITY.
FT DISULFID 1333 1348 BY SIMILARITY.
FT DISULFID 1350 1361 BY SIMILARITY.
FT DISULFID 1367 1380 BY SIMILARITY.
FT DISULFID 1374 1389 BY SIMILARITY.
FT DISULFID 1391 1402 BY SIMILARITY.
FT DISULFID 1408 1420 BY SIMILARITY.
FT DISULFID 1415 1429 BY SIMILARITY.
FT DISULFID 1450 1461 BY SIMILARITY.
FT DISULFID 1456 1470 BY SIMILARITY.
FT DISULFID 1472 1485 BY SIMILARITY.
FT DISULFID 1491 1502 BY SIMILARITY.
FT DISULFID 1497 1511 BY SIMILARITY.
FT DISULFID 1513 1526 BY SIMILARITY.
FT DISULFID 1610 1622 BY SIMILARITY.
FT DISULFID 1617 1631 BY SIMILARITY.
FT DISULFID 1633 1646 BY SIMILARITY.
FT DISULFID 1652 1663 BY SIMILARITY.
FT DISULFID 1658 1672 BY SIMILARITY.

DB 135 --RVSQD--CHNLPSGYOCTCHDYRKGIGPE--CVDIDECRYRYCQHRKCVNI.PGSPKOC- 188
 QY 172 SPGLQADGRTCDVDDECATGRASCPFRFCQYNTFGSYICKCHKGFDLMVIGKYOCHD 231
 DB 189 EYCHQGLPNKRSQVDFNECDMG--AICWQRCNSVGTFLCRCHQGYELHRDG--FSCSD 243
 QY 232 IDECSLQYQCCSPARCYNVNGSYKCKCKPGYQ-----GGGICTCV 271
 DB 244 IDECSYSSYLQ--YRCVNEPGRFSCHCPOGYQLLATRLCQIDECESGAIQCSEAGTCV 301
 QY 272 YIPKVMIEPSPHVPKGNCTILKQDTGNWNIIDVGVSTWHPKTPYIPVITNR---PT 328
 DB 302 NF-----HOGYRCVDIT--NRV-----EPYI-QVSNRRCICPA 331
 QY 329 SKPTRTPTKPTPIPTPPPPPTLPLPTTPTTPTTGLTIAPMASTPPGGITVD 368
 DB 332 SNPLCRKQ-----PSSIVHYMYMTITSKRSVPADVFOIAISVYPGAY--- 373
 QY 389 NRQVTDQPKPRGVDFIPRPSN 410
 DB 374 NAFQIRAGNSQGFYI-RQINN 394

RESULT 10

FB14_CRIGR STANDARD; PRT: 443 AA.
 AC 025058;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
 DE (Fibulin-4) (FBLN-4) (H411 protein).
 GN EFEMP2 OR FBLN4.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Heine H., Delude R.L., Monks B., Golenbock D.T.;
 RI Submitted (FEH-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF046870; AAC03101.1;
 DR HSSP: P00736; IAPQ.
 DR InterPro: IPR000152; Asx_hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_Ca.
 DR Pfam: PF00008; EGF_4.
 DR SMART: SM00179; EGF_CA; 4.
 DR SMART: SM00001; EGF-like; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 4.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; 4.
 DR PROSITE: PS01187; EGF_CA; 6.
 KW Repeat: EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL
 FT CHAIN 1 25
 FT 26 443
 FT EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT FT
 FT DOMAIN 36 81
 FT DOMAIN 123 163
 FT EGF-LIKE 1, DIVERGENT.
 FT EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT

FT DOMAIN 164 202
 FT DOMAIN 203 242
 FT DOMAIN 243 282
 FT DOMAIN 283 328
 FT DISULFID 127 140
 FT DISULFID 141 149
 FT DISULFID 151 162
 FT DISULFID 168 177
 FT DISULFID 173 186
 FT DISULFID 188 201
 FT DISULFID 207 217
 FT DISULFID 213 226
 FT DISULFID 228 241
 FT DISULFID 247 258
 FT DISULFID 254 267
 FT DISULFID 269 281
 FT DISULFID 287 300
 FT DISULFID 294 309
 FT DISULFID 315 327
 FT CARBOHYD 198
 FT CARBOHYD 394
 SQ SEQUENCE 443 AA; 49432 MW; 0BCE5D732D9E5F CRC64;
 Query Match 10.5%; Score 346.5; DH 1; Length 443;
 Best local Similarity 36.8%; Pred. No. 2.8e-14;
 Matches 77; Conservative 31; Mismatches 68; Indels 44; Gaps 12;
 QY 76 VCPGCK-----HGECIGP-----NKCKPGY---AGKTCIGVINEGKLPKPK 118
 DB 79 ICUPRRAAVINDIHRG--GPPPPVPAQHNPDPYDFPDRSVVDV DEAGALHHRK 145
 QY 119 --HRCNNTYGSYKCYGNGYMLM--PDGSSSALITCSMANCYGCHVVKQIRGQFISPHL 175
 DB 136 PSQDCHNLPGSYGCTCPDGYRKVGPE--CVDIDECRYRYCQHRKCVNI.PGSPKOC EPGF 192
 QY 176 QIAPDCHTCDVDDECATGRASCPFRFCQYNTFGSYICKCHKGFDLMVIGKYOCHD 243
 DB 193 QIGPNRNSQVDFNECDMG--AICWQRCNSVGTFLCRCHQGYELHRDG--FSCSD 247
 QY 236 SLGQYCCSFARCYNVNGSYKCKCKEGYQ 264
 DB 248 SYSSYLQ--YRCVNEPGRFSCHCPOGYQ 274

RESULT 11

FBL1_HUMAN STANDARD; PRT: 703 AA.
 ID FBL1_HUMAN
 AC P23142; P23143; P23144; P37888; Q40GR4;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibulin-1 precursor.
 GN FBLN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RX MEDLINE: 91100426; PubMed: 2269669;
 RA Agraves W.S., Tran H., Hargess W.H., Dickerson K.;
 RT *Fibulin is an extracellular matrix and plasma glycoprotein with
 RT repeated domain structure.*;
 RL J. Cell Biol. 111:3155-3164(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM D).
 RA Agraves S.;
 RI Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 567-703 FROM N.A. (ISOFORM C).
 RA Connor R.;
 RI Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE OF 30-44.
 RA MEDLINE=89354537; PubMed-2527614;
 RA Argraves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;
 RT "Fibulin, a novel protein that interacts with the fibronectin
 RT receptor beta subunit cytoplasmic domain.";
 RL Cell 58:623-629(1989).
 CC -!- SUPRACELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A, B, C AND D (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER ONLY IN THEIR C-
 CC TERMINAL REGIONS.
 CC -!- SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: X53741; CAA37770.1; -;
 DR EMBL: X53742; CAA37771.1; -;
 DR EMBL: X53743; CAA37772.1; -;
 DR EMBL: U01244; AAB17099.1; -;
 DR EMBL: Z95331; CAB62960.1; -;
 DR PIR: A32826; A32826.
 DR PIR: A36346; A36346.
 DR PIR: B36346; B36346.
 DR PIR: C36346; C36346.
 DR HSSP: P35555; 1PMN.
 DR Genew: HGNC:3600; FBLN1.
 DR MIM: 135820; -;
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001881; EGF_CA.
 DR Pfam: PF00008; EGF; 6.
 DR Pfam: PF01821; ANATO; 3.
 DR SMART: SM00104; ANATO; 3.
 DR SMART: SM00179; EGF_CA; 7.
 DR SMART: SM00001; EGF_Like; 2.
 DR PROSITE: PS00010; ASX_HYDROXYL; 4.
 DR PROSITE: PS00022; EGF_L1; FALSE_NEG.
 DR PROSITE: PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 8.
 KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
 KW Repeat; EGF-like domain; Calcium-binding.
 FT SIGNAL 1 29
 FT CHAIN 30 703
 FT DOMAIN 36 76 FIBULIN-1.
 FT DOMAIN 77 111 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 112 144 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 176 215 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 216 261 EGF-LIKE 1.
 FT DOMAIN 262 307 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 308 355 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 356 398 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 399 440 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 441 480 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 481 524 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 525 578 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 36 61 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 37 68 BY SIMILARITY.
 FT DISULFID 50 69 BY SIMILARITY.
 FT DISULFID 78 109 BY SIMILARITY.
 FT DISULFID 91 110 BY SIMILARITY.
 FT DISULFID 112 136 BY SIMILARITY.
 FT DISULFID 113 143 BY SIMILARITY.
 FT DISULFID 126 144 BY SIMILARITY.
 FT DISULFID 180 190 BY SIMILARITY.

FT DISULFID 186 199 BY SIMILARITY.
 FT DISULFID 201 214 BY SIMILARITY.
 FT DISULFID 220 233 BY SIMILARITY.
 FT DISULFID 227 242 BY SIMILARITY.
 FT DISULFID 248 260 BY SIMILARITY.
 FT DISULFID 266 279 BY SIMILARITY.
 FT DISULFID 273 288 BY SIMILARITY.
 FT DISULFID 294 306 BY SIMILARITY.
 FT DISULFID 312 325 BY SIMILARITY.
 FT DISULFID 319 334 BY SIMILARITY.
 FT DISULFID 341 354 BY SIMILARITY.
 FT DISULFID 360 373 BY SIMILARITY.
 FT DISULFID 367 382 BY SIMILARITY.
 FT DISULFID 384 397 BY SIMILARITY.
 FT DISULFID 403 415 BY SIMILARITY.
 FT DISULFID 411 424 BY SIMILARITY.
 FT DISULFID 426 439 BY SIMILARITY.
 FT DISULFID 445 454 BY SIMILARITY.
 FT DISULFID 450 463 BY SIMILARITY.
 FT DISULFID 465 479 BY SIMILARITY.
 FT DISULFID 485 498 BY SIMILARITY.
 FT DISULFID 494 507 BY SIMILARITY.
 FT DISULFID 509 523 BY SIMILARITY.
 FT DISULFID 529 542 BY SIMILARITY.
 FT DISULFID 536 551 BY SIMILARITY.
 FT DISULFID 556 577 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 539 539 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 567 703 MISSING (IN ISOFORM A).
 FT VARSPPLIC 567 601 LQEKTDTRCIRKSCRENDVTCVDPVHTTISHIVI -> OK
 FT SKKQNTIPAGSKEDKCVLPWKQGLDTHIDA (IN
 FT ISOFORM B).
 FT VARSPPLIC 567 703 LQEKTDTRCIRKSCRENDVTCVDPVHTTISHIPLTER
 FT EFTPEELIFLRAITPPASQANIIFDIETGNLRDSEFII
 FT KRYMDGTVGVQVRPIVGPFAVLKLENNYVGVGVSRR
 FT NVNVRIFVSYWF -> KCHRLPCHENRCKSKLPIRTYY
 FT HLPPTNIOAPVAFVPMGPPSAVPGDSMQIAITGNPEFGFF
 FT TTRKVSHPGVAULTKVPPEPROLLTVMKMLSRHGTVSFF
 FT VAKLFIIVSAEL (IN ISOFORM C).
 FT C -> S (IN REF. 4).
 FT CONFLICT 36 36 HR -> SH (IN REF. 4).
 FT CONFLICT 41 42
 FT SEQUENCE 703 AA; 77274 MW; EFD88465BA2D3A25 CRC64;
 Query Match 10.4%; Score 343; DB 1; Length 703;
 Best Local Similarity 26.7%; Pred. No. 6.4e-13;
 Matches 106; Conservative 43; Mismatches 118; Indels 130; Gaps 20;
 QY 31 SSIGLCRYGGRIDCCGWAKRWSGQC-----QPFYVLKQRIAR 68
 DB 281 NTLGSFRCPKLOQKSGFIQDAGLNCIDINECLISAPCPIGHTCINTEGSYTCNNVPN 340
 QY 69 -----IRCOLKAVCOP---RCKHG-ECI---GNKCKCHPGY---AGTKCIQV 106
 DB 341 CGRGYHNEGTCTVDVDECAPPAEPCGKHGKCVNSPGFCECKTGYTFYFCISRMCDIV 400
 QY 107 LNECGKLP-RPCKHRCMNTYGYKCYCLNGYMLMPDG-SCSSALTCSSMANCYGCDVYVK 164
 DB 401 -NECQYFGRLGCHKCENTLSYLCSCSVGFLSVDRSCEDINECSSPSCQECANYVG 459
 QY 165 QIRQCPSPIQLAP-DGRTCVDDVECA--TCRASCPHRCQVNTFGSYICKK-HKGFDI. 220
 DB 460 SYQCYC-RRGYLSVDGVTCEDICALPTGGHICS--YRCINIPGSGQSCPSGGYRL 516
 QY 221 MYIGKYCHDIDECSLGYOCSSFARCYNVVRSYKCY---KCKEY----- 263
 DB 517 APNG--RNCQDIDECVTGIHNCININETCFNIOGACRCLAFCEPENYKSAATLQOKKTD 574
 QY 264 -----QQDGLTCVYIPKVMIEPSPGIHVPKNGTILKGDGTGNNNWIPDVGSTWPPKT 316
 DB 575 VRCKISCRENDVTCVF-----DPVIT----- 595
 QY 317 PYIPPIITNRPTSKPTTRTPKPTPI-----PTPPP 348

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DB 596 -----ISHTVISLPTRETPREHIFLRAITPPHP 626
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RESULT 12
PHIL_CHICK STANDARD; PRT; 684 AA.
AC Q7375;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibulin-1 precursor.
CN PHIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120531; PubMed=9923656;
RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
RT "Identification of chicken and C. elegans fibulin-1 homologs and
RT characterization of the C. elegans fibulin-1 gene.";
RL Matrix Biol. 17:635-646(1998).
CC -! SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -! SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
CC -! SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
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CC -----
CC EMBL: AC051400; AAC05388.1;
CC HSSP: P00742; IHGG.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR Pfam: PF00008; EGF; 6.
DR Pfam: PF01821; ANATO; 2.
DR Pfam: SM00104; ANATO; 3.
DR SMART: SM00179; EGF_CA; 8.
DR SMART: SM00001; EGF_Like; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 5.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 2.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 8.
KW Signal; Glycoprotein; Extracellular matrix; Repeat; EGF-like domain;
KW Calcium-binding.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 684 FIBULIN-1.
FT DOMAIN 33 74 ANAPHYLATOXIN-LIKE 1.
FT DOMAIN 75 109 ANAPHYLATOXIN-LIKE 2.
FT DOMAIN 110 142 ANAPHYLATOXIN-LIKE 3.
FT DOMAIN 177 216 EGF-LIKE 1.
FT DOMAIN 217 262 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 263 308 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 309 356 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 357 399 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 400 441 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 442 481 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 482 525 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 526 570 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DISULFID 33 59 BY SIMILARITY.
FT DISULFID 34 66 BY SIMILARITY.
FT DISULFID 47 67 BY SIMILARITY.

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FT DISULFID 76 107 BY SIMILARITY.
FT DISULFID 89 108 BY SIMILARITY.
FT DISULFID 110 134 BY SIMILARITY.
FT DISULFID 111 141 BY SIMILARITY.
FT DISULFID 124 142 BY SIMILARITY.
FT DISULFID 181 191 BY SIMILARITY.
FT DISULFID 187 200 BY SIMILARITY.
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FT DISULFID 221 234 BY SIMILARITY.
FT DISULFID 228 243 BY SIMILARITY.
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FT DISULFID 274 289 BY SIMILARITY.
FT DISULFID 295 307 BY SIMILARITY.
FT DISULFID 313 326 BY SIMILARITY.
FT DISULFID 330 335 BY SIMILARITY.
FT DISULFID 342 355 BY SIMILARITY.
FT DISULFID 361 374 BY SIMILARITY.
FT DISULFID 368 383 BY SIMILARITY.
FT DISULFID 385 398 BY SIMILARITY.
FT DISULFID 404 416 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.
FT DISULFID 427 440 BY SIMILARITY.
FT DISULFID 446 455 BY SIMILARITY.
FT DISULFID 451 464 BY SIMILARITY.
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FT DISULFID 495 508 BY SIMILARITY.
FT DISULFID 510 524 BY SIMILARITY.
FT DISULFID 530 543 BY SIMILARITY.
FT DISULFID 537 552 BY SIMILARITY.
FT DISULFID 557 569 BY SIMILARITY.
FT CARBOHYD 96 96 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 536 536 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 540 540 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 638 638 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 684 AA; 75623 MW; 163807A094739199 CRC64;

Query Match 10.1%; Score 343.5; DB 1; Length 684;
Best Local Similarity 40.0%; Pred. No. 2.2e 12;
Matches 86; Conservative 24; Mismatches 80; Indels 25; Gaps 17;

QY 78 QPCKHGE-CI-CPN--KCKCHGYA----GKTCIQVINEGGLKP RCKKHKMNTYASY 128
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 366 QP-CGEGHYVINGPNYRCECKSGYSFVSRCTDI-NEKRYRGLCAHKCENTPGSY 424
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 129 KCYCLNGYMLPDG-SCSSALTCSMANQYGGVYKQIRCCQSPSGQLQAP DERTVVD 186
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 424 YCTCIMGPKLSSNGRSCDLINESSPCSCQCANVYGVOCYC-RGFQSLDGLSLED 482
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 187 VDECA--TGRASCPRQCQVNTFGSYKCG-IKGFQDMVIGKYQCHIDIDECISLQYQCS 244
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 IDECALPTGCHIC-SFR-CINIPGSFQCTPSTGYRL-APNARNQGDIDECVAETHNCS 548
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 SFARCVNVCSYKVC---KCKFGYOGIGLT-CVYIP 274
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 539 FNETCFNIQGFRCLSLECPENTYKSGDTRCERLP 573
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
PHIL_MOUSE
ID PHIL_MOUSE STANDARD; PRT; 443 AA.
AC Q9WVJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
DE (Fibulin-4) (FBLN-4) (Mutant p53 binding protein 1).
GN EFEMP2 OR FBLN4 OR MBP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

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FT DISULFID 138 153 BY SIMILARITY.
FT DISULFID 155 166 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 177 190 BY SIMILARITY.
FT DISULFID 192 205 BY SIMILARITY.
FT DISULFID 211 221 BY SIMILARITY.
FT DISULFID 217 230 BY SIMILARITY.
FT DISULFID 232 245 BY SIMILARITY.
FT DISULFID 251 262 BY SIMILARITY.
FT DISULFID 258 271 BY SIMILARITY.
FT DISULFID 273 286 BY SIMILARITY.
FT DISULFID 292 305 BY SIMILARITY.
FT DISULFID 299 314 BY SIMILARITY.
FT DISULFID 320 332 BY SIMILARITY.
FT CARBOHYD 283 283 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 448 AA; 50193 MW; F15CC70CCFBDC97 CRG64;

Query Match 10.0%; Score 330.5; DB 1; Length 448;
Best Local Similarity 40.0%; Pred. No. 2.3e-12;
Matches 70; Conservative 18; Mismatches 72; Indels 15; Gaps 8;

QY 94 CHPGY---AGKTCIQVLNEGGLKPRCK--HRCMNTYGSYKCYCLNGYMLMPDGCSSAL 148
Db 113 CRFGYQNDGEGNOCVDV-DECATDSDHCNPTQICINTEGGYTCSTDGYWLL-EGQCLDID 170

QY 149 TCSMANCOYGDVVVKQIRQCPSGLQIAPDGRTCVDVDECATGRASCPHFQCVNTFG 208
Db 171 ECRYGYCQQLCANVPGSYSCTC-NPGFTLNDGRSCODVNECETEN---PCVQTCVNTYG 226

QY 209 SYICKCHKGFDLMYIGGKYOCHDIDEGSLGYQCSSFARCYNVRGSYKCKCKEGY 263
Db 227 SFICRCDPGYELEDG--IHCSMDGCSFSEFLCQH--ECVNQPGSYFCSCPPGY 277
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Search Completed: April 23, 2003, 13:01:36
Job time : 26 secs

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